

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:09:34 ; Search time 299.73 Seconds
(without alignments)
16.424 Million cell updates/sec

Title: US-09-331-631A-8_COPY_120_161
Perfect score: 245
Sequence: 1 SORPQECQHCHQOORPE.....QQVRECEKRYQENPWRCR 42

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:REMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111.5	45.5	525	10 Q43358	Q43358 theobroma c
2	103	42.0	593	10 Q9SEW4	Q9SEW4 juglans reg
3	98	40.4	625	10 Q9SP13	Q9SP13 macadamia i
4	98	40.0	666	10 Q9SP14	Q9SP14 macadamia i
5	94	38.4	666	10 Q9SP15	Q9SP15 macadamia i
6	91	37.1	393	10 Q9ZTP0	Q9ZTP0 oryza sativ
7	74	30.2	900	5 Q9VK09	Q9VK09 drosophila
8	74	30.2	3828	5 Q24742	Q24742 drosophila
9	72.5	29.6	402	10 Q9ZRH8	Q9ZRH8 oryza sativ
10	72	29.4	425	5 Q17400	Q17400 caenorhabdi
11	72	29.4	600	5 Q17401	Q17401 caenorhabdi
12	70	28.6	637	10 Q03678	Q03678 hordeum vul
13	70	28.6	905	5 Q18260	Q18260 caenorhabdi
14	69.5	28.4	328	5 Q9VE66	Q9VE66 drosophila
15	69.5	28.4	925	5 Q9V7C5	Q9V7C5 drosophila
16	69	28.2	2123	5 Q9U9S7	Q9U9S7 dictyosteli
17	68	27.8	57	4 Q9Y4J1	Q9Y4J1 homo sapien
18	68	27.8	930	10 Q9S2Y9	Q9S2Y9 arabidopsis
19	67.5	27.6	709	5 Q9N4R2	Q9N4R2 caenorhabdi

20	66.5	27.1	152	10 Q41168	Q41168 raphanus sa
21	66.5	27.1	174	10 Q41169	Q41169 raphanus sa
22	66	26.9	279	11 Q35846	Q35846 mus musculu
23	66	26.9	815	4 Q9UJG2	Q9UJG2 homo sapien
24	65.5	26.7	178	10 Q96339	Q96339 brassica ca
25	65.5	26.7	1457	5 Q9VT35	Q9VT35 drosophila
26	65	26.5	259	5 Q9W483	Q9W483 drosophila
27	65	26.5	388	5 Q16500	Q16500 caenorhabdi
28	65	26.5	388	5 Q16501	Q16501 caenorhabdi
29	65	26.5	419	5 Q9NA38	Q9NA38 caenorhabdi
30	65	26.5	420	5 Q9NA61	Q9NA61 caenorhabdi
31	65	26.5	438	5 Q16502	Q16502 caenorhabdi
32	65	26.5	445	5 Q16511	Q16511 caenorhabdi
33	64.5	26.3	411	5 P91419	P91419 caenorhabdi
34	64.5	26.3	425	5 Q15755	Q15755 dictyosteli
35	64	26.1	129	2 Q9RNE4	Q9RNE4 streptococc
36	64	26.1	242	5 Q19919	Q19919 caenorhabdi
37	64	26.1	549	5 Q9VF63	Q9VF63 drosophila
38	64	26.1	687	3 P87065	P87065 candida alb
39	64	26.1	838	5 Q27422	Q27422 caenorhabdi
40	64	26.1	838	5 Q18761	Q18761 caenorhabdi
41	64	26.1	1068	5 Q9W539	Q9W539 drosophila
42	64	26.1	1464	5 Q96836	Q96836 drosophila
43	64	26.1	3583	5 Q9V3N4	Q9V3N4 drosophila
44	64	26.1	3584	5 Q9U999	Q9U999 drosophila
45	63.5	25.9	101	5 Q9TVK8	Q9TVK8 drosophila

ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	525 AA.
Q43358	Q43358	01-NOV-1996 (TREMBLrel. 01, Created)		
AC	Q43358	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	VICILIN PRECURSOR.			
GN	CSV			
OS	Theobroma cacao (Cacao).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;			
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;			
OC	Malvales; Malvaceae; Theobroma.			
OX	NCBI_TaxID=3641;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LEAVES;			
RX	MEDLINE=92288309; PubMed=1600151;			
RA	McHenry L., Fritz P.J.;			
RT	*Comparison of the structure and nucleotide sequences of vicilin genes			
RT	of cocoa and cotton raise questions about vicilin evolution.*;			
RL	Plant Mol. Biol. 18:1173-1176(1992).			
DR	EMBL: X62625; CAA4493.1; -.			
DR	EMBL: X62626; CAA4494.1; -.			
DR	HSSP: P02853; 2PHL.			
DR	MENDEL: 30919; Thecc:1188;30919.			
DR	INTERPRO: IPR001113; -.			
DR	PFAM: PF00546; Seedstore_7s; 1.			
DR	PRODOM: PD081059; -; 1.			
KW	Signal.			
FT	SIGNAL			
FT	CHAIN			
SO	SEQUENCE			

Query Match 45.5%; Score 111.5; DB 10; Length 525;

Best Local Similarity 50.0%; Pred. No. 6.8e-06; Mismatches 10; Indels 1; Gaps 1;

QY 2 OROFQECQHCHQOORPEKKQOCVRECKRYQENPWRCR 41
DB 82 OROYQOCQGRCEQOQOQOREQOQOCRKWEYKEOE-RGE 120

RESULT	2	
09SEW4		
ID	09SEW4	PRELIMINARY; PRT; 593 AA.
AC	09SEW4	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)	
DE	VICLIN-LIKE PROTEIN PRECURSOR (FRAGMENT).	
OS	Juglans regia (English walnut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;	
OC	Fagales; Juglandaceae; Juglans.	
OX	NCBI_TaxID=51240;	
RX	[1]	
RP	SEQUENCE FROM N.A.	
RA	STRAIN=CV, SUNDLAND; TISSUE=SONATIC EMBRYO LINE;	
RA	Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;	
RT	"Identification and cloning of a cDNA encoding a vicilin-like protein,	
RT	Jug r 2, from English walnut kernel (Juglans regia): a major food	
RT	allergen."	
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; AF0606055; AAF18269.1; -.	
DR	HSSP; P02853; 2PHL.	
DR	INTERPRO; IPR001113; -.	
DR	PFAM; PF00546; Seedstore_75; 1.	
FT	NON_TER	
SO	SEQUENCE	593 AA; 69990 MW; 9BA127E19B18C0D8 CRC64;

	Query Match	Similarity	Score	DB	Length
Best Local	42.0%	42.1%	103	10	593
Matches	16	Conservative	9	Mismatches	11
				Indels	0
				Gaps	0

FT	SEQUENCE	625 AA: 73586 MW: 415808AB9D370296 CRC64:
Q0	NON_TER	1
DR	PFAM: PF00546; Seedstore-7s; 1.	
DR	INTERPRO: IPR001113; -	
DR	HSSP: P02853; 2PHL.	
DR	EMBL: AF161885; AAD54246.1; -	
RL	Plant J. 0:0-0(1999).	
RT	globulin protein in Macadamia integrifolia.";	
RT	Macus J.P., Goulter K.C., Green J.L., Manners J.M.;	
RA	"A family of antimicrobial peptides is produced by processing of a 7S	
RC	TRISSE=NUIT KERNAL.	
RP	SEQUENCE FROM N.A.	
RN	NCBI_Taxid=60698;	
OX	11	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
GN	AMP2.	
DE	VICILIN PRECURSOR (FRAGMENT).	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, last annotation update)	
DE	VICILIN PRECURSOR (FRAGMENT).	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
GN	AMP2.	
DE	VICILIN PRECURSOR (FRAGMENT).	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, last annotation update)	
DE	VICILIN PRECURSOR (FRAGMENT).	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
GN	AMP2.	
DE	VICILIN PRECURSOR (FRAGMENT).	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, last annotation update)	
DE	VICILIN PRECURSOR (FRAGMENT).	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
GN	AMP2.	
DE	VICILIN PRECURSOR (FRAGMENT).	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, last annotation update)	
DE	VICILIN PRECURSOR (FRAGMENT).	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
GN	AMP2.	
DE	VICILIN PRECURSOR (FRAGMENT).	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, last annotation update)	
DE	VICILIN PRECURSOR (FRAGMENT).	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
GN	AMP2.	
DE	VICILIN PRECURSOR (FRAGMENT).	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, last annotation update)	
DE	VICILIN PRECURSOR (FRAGMENT).	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
GN	AMP2.	
DE	VICILIN PRECURSOR (FRAGMENT).	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, last annotation update)	
DE	VICILIN PRECURSOR (FRAGMENT).	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
GN	AMP2.	
DE	VICILIN PRECURSOR (FRAGMENT).	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, last annotation update)	
DE	VICILIN PRECURSOR (FRAGMENT).	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
GN	AMP2.	
DE	VICILIN PRECURSOR (FRAGMENT).	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, last annotation update)	
DE	VICILIN PRECURSOR (FRAGMENT).	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	
OC	Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.	
GN	AMP2.	
DE	VICILIN PRECURSOR (FRAGMENT).	
DT	01-MAY-2000 (TReMBLrel. 13, Created)	
DT	01-MAY-2000 (TReMBLrel. 13, last sequence update)	
DT	01-OCT-2000 (TReMBLrel. 15, last annotation update)	
DE	VICILIN PRECURSOR (FRAGMENT).	
GN	AMP2.	
OS	Macadamia integrifolia (Macadamia nut).	
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	</

Query Match	40.48;	Score 99;	DB 10;	Length 625;
Best Local Similarity	38.38;	Pred. No. 0.00025;		
Matches 18;	Conservative 11;	Mismatches 8;	Indels 10;	Gaps 2;
0y	2	QRPQECQDCHQDEQREKKQDCVREKREKQE-----NPMRG	40	

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Db      150 QREYEDCRHCEQEE--PRLQYQCRQCEQQRQHGSGDLMNPQRG 194

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RESULT	4	09SP14	PRELIMINARY:	PRT:	666 AA.
ID	09SP14				
AC	09SP14:				
DT	01-MAY-2000	(TREMBLrel, 13, Created)			
DT	01-MAY-2000	(TREMBLrel, 13, Last sequence update)			
DT	01-OCT-2000	(TREMBLrel, 15, Last annotation update)			
DE	VITILIN PRECURSOR.				
GN	AMP2.				
OS	Macadamia integrifolia (Macadamia nut).				
OC	Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:				
OC	Maenillophyta: eudicotyledons: Proteaceae: Macadamia.				
OX	NCBI_TaxID=60698;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=NUC KERNEL;				
RA	Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;				
RT	"A family of antimicrobial peptides is produced by processing of a 75S				
RL	gliobulin protein in Macadamia integrifolia.";				
RL	plant J. 0:0-0(1999).				
DR	EMBL: AF161884; AAD54245.1; -.				
DR	HSSP: P02853; 2PHL.				
DR	INTERPRO: IPR001113; -.				
DR	PRAM: PF00546; Seedstote.7s; 1.				
SO	SEQUENCE 666 AA: 78243 MW: 06CA22F8710F8A7B CRC64;				

```

Query Match Similarity      40.0%; Score 98; DB 10; Length 666;
Best Local Similarity      38.3%; Pred No. 0.00035;
Matches    18; Conservative   11; Mismatches    8; Indels   10; Gaps    2.

QY      2 QKQFECOOHC HQEQRPEKKQCVCRECKRYQE-----NPMRG 40
          |||::|||::|||::|||::|||::|||::|||::|||
Db     191 GREYEDCRRCRCEOE--PROOYCCHRCRCEORHGRGDLINPORG 235
          |||::|||::|||::|||::|||::|||::|||::|||

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RESULT 5
O9SP.L5
ID O9SP.L5 PRELIMINARY; PRT; 666 AA.
AC O9SP.L5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE VITILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; Proteaceae; Macadamia.
OX NCBI_TaxID=60696;
RX 11
RN SEQUENCE FROM N.A.
RP TISSUE=NUT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;
RT "A family of antimicrobial peptides is produced by processing of a 7S
RT plantulin protein in Macadamia integrifolia kernels.";
RL Plant J. 0:0-0(1999).
DR EMBL; AF161883; AAD54244.1; -.
DR HSSP; P02853; 2P.HL.
DR INTERPRO: IPR001113; -.
DR PfAM; PF00546; Seedstore_7s; 1.
SO SEQUENCE 666 AA; 78217 MW; C752B084B2DF0224 CRC64;

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	Query Match	38.4%	Score 94;	DB 10;	Length 666;
	Best Local Similarity	35.3%;	Pred. No.	0.0011;	
Matches	12; Conservative	11;	Indels	0;	Gaps 0;
OY	2 ORDFECGQHCHQCEOREPEKKQCVRREKRYOE 35 ::: :: : :				

AC 092RRH-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE EARLY EMBRYOGENESIS PROTEIN.
GN OSE362.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, TAINUNG 67;
RA Tseng M.J., Wang C.S., Hsu H.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U25969; AAD10370.1; -;
SQ SEQUENCE 402 AA; 44252 MW; F03C86948F840060 CRC64;

Query Match 29.6%; Score 72.5; DB 10; Length 402;
Best Local Similarity 39.5%; Pred. NO. 0.27;
Matches 15; Conservative 8; Mismatches 6; Indels 9; Gaps 3

```
QY      6 QECQQHC-HDEQRPEKKQOCVAECREKTYQENPMGER 42
          |::|::|||::|:|
Db    252 QQCRKQCQHNNHD--WKKQCSMDCRQ-----WRRR 281
```

RESULT	10			
017400				
ID	017400	PRELIMINARY;	PRT;	425 AA.
AC	017400;			
DT	01-JAN-1999 (TrEMBLrel. 09, Created)			
DT	01-JAN-1999 (TrEMBLrel. 09, Last sequence update)			
DT	01-JAN-1999 (TrEMBLrel. 09, Last annotation update)			
DE	HYPOTHETICAL 45.9 KDA PROTEIN AC3.3 IN CHROMOSOME V PRECURSOR.			
GN	AC3.3			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;			
OC	Rhabditidae; Peloderinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BRISTOL N2;			
RA	McMurray A.;			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
CC	1- SIMILARITY: BELONGS TO FAMILY UPE.			
DR	EMBL: Z71177; CAA94867.1; -.			
DR	MORSEP; AC3.3; CE05133.			
KW	Hypothetical protein; Signal.			
FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	425	HYPOTHETICAL PROTEIN AC3.3.
SQ	SEQUENCE	425 AA;	45922 MW;	9513552AZAFET996C CRC64;

[illegible]

RESULT	11	
017401		
017401		
ID	017401	PRELIMINARY;
AC	017401	PRT; 600 AA.
DT	01-JAN-1999	(TIMBLrel. 09, Created)
DT	01-JAN-1999	(TIMBLrel. 09, Last sequence update)
DT	01-JUN-2000	(TIMBLrel. 14, Last annotation update)
DE	HYPOTHEITICAL 67.7 KDA PROTEIN AC3.4 IN CHROMOSOME V	
	AC3.4.	

OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea
OC Rhabditidae; Peloiderinae; Caenorhabditis.
OX NCBI_taxid=6239;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-BRISPOL N2;
RA Mcmurray A.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO FAMILY UFP.
DR EMBL: Z71177; CA94868.1; -.
DR MORPEP: AC3.4; CE05134.
DR INTERPRO: IPR001594; -.
DR PFM: PFO1529; zF-DHHC; 1.
DR PRODOM: PD003041; -. 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 309 329 POTENTIAL.
FT TRANSMEM 447 467 POTENTIAL.
FT TRANSMEM 490 510 POTENTIAL.
FT DOMAIN 6 287 GLN-RICH.
SQ SEQUENCE 600 AA; 67740 MW; 504A5CE1BA72091B CRC64;

Query Match	29.48;	Score 72;	DB 5;	Length 600;
Best Local Similarity	46.48;	Pred. No. 0.44;		
Matches 13;	Conservative 7;	Mismatches 4;	Indels 4;	Gaps 1;

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OY      6 QECQHCCHQ-----QEORPEKKQQCVREC 29
          | : | | | | | : : : | | | : |
Db     24 QQCQCCVCVQTPIQQCQPQCQCQCVCVQC 51
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RESULT	12		
003678			
ID	003678	PRELIMINARY;	PRF; 637 AA.
AC	003678;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	FETAL STORAGE PROTEIN.		
GN	BEG1 OR GBL.		
OS	Hordeum vulgare (Barley), and Triticum aestivum (Wheat).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta.		
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.		
OX	NCI_TaxID=4513, 4565;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=93287988; PubMed=8510647;		
RA	Heck G.R., Chamberlain A.C., Ho T.H.D.;		
RT	"Barley embryo globulin 1 gene, Beg1: characterization of cDNA,		
RT	chromosome mapping and regulation of expression.";		
RL	Mol. Gen. Genet. 239:209-218(1993).		
RL	EMBL: M64372; AAA32936.1; -;		
DR	EMBL: M81715; AAA34265.1; -;		
DR	HSSP: P02853; 2PHT.		
DR	MEDEL: 8553; Horvu;1188;8553.		
DR	INTERPRO: IPR000901; -;		
DR	INTERPRO: IPR001113; -;		
DR	PFAM: PF00546; Seedstore_7s; 1.		
DR	PROSITE: PS00867; CPASL2; UNKNOWN_1.		
DR	PRODOM: PD081059; -; 1.		
QW	Seed storage protein.		
QW	SEQUENCE 637 AA; 72252 MW; F323FAFF99947C3C CRC64;		

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Query Match      28.6%  Score 70: DB 10; Length 637;
Best Local Similarity 30.6%  Pred No. 0.8;
Matches 15; Conservative 7; Mismatches 13; Indels 14; Gaps 2

OY      6 QECQCHQHOEORPEKKOOCVRECKREKYOEN-----PWRCG 41
          : : : : : : : : : : : : : : : : : : : :
bb      42 OOCVARRCROEPRR-YSNARCVCEDRDDOOGRHNEOEOEGRGWNGE 89
          : : : : : : : : : : : : : : : : : : : :

```

us-09-331-631a-8_copy_120_161.rspt

OC Pharyngota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha,
OC Ephyraoidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Lewis R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Asgharai A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Bagayati A., Baxendale J., Bayraktaroglu B., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burtils K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Paolos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Haverty D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
RA Jaisl M., Kalush F., Kappen G.H., Ke Z., Kennison J.A., Kethum K.A.,
RA Kimmel B., Lei Y., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Malshina N.V., Mobarry C., Morris J., Mostrelf A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sidenkiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*.",
RL Science 287:2125-2195(2000).
DR EMBL: AE003722; AAF55563.1; -.
DR HSSP: P17789; 2DRP.
DR FLYBASE: FBgn0038624; CG14307.
DR INTERPRO: IPR000822; -.
DR PFAM: PF000096; z1-C2H2; 1.
DR PROSITE: PS000028; ZINC_FINGER_C2H2; 1.

		28.4%;	Score	69.5;	DB	5;	Length	328;
Berry March		36.6%;	Pred.	No.	0.51;			
Best Local Similarity		10;	Mismatches	13;	Indels	3;	Gaps	1.
Matches	15;	Conservative						
OY	2	QROFEOCCHOCDOEOPREKKOQCVCREKRY--	-OEENPWR	39				
	I:I I : IIII:::	:II :	:	:I II				
Dd	115	QQQQQQQQHHQHQQHQHQQSQQQQQQHHQLGMNNGAMR	155					
RESULT	15							
ID	Q9V7C5							
Q9V7C5		PRELIMINARY:		PRT:	925 AA.			
AC	Q9V7C5:							
DI	01-MAY-2000	(TREMBLrel. 13,	Created)					
DT	01-MAY-2000	(TREMBLrel. 13,	Last sequence update)					
DF	01-MAY-2000	(TREMBLrel. 13,	Last annotation update)					
DE	Cgi2964	PROTEIN.						
GN	Cgi2964.							
GS	Drosophila melanogaster	(fruit fly).						

